

#6

SEQUENCE LISTING



<110> MIZUTANI, Masako
TANAKA, Yoshikazu
KUSUMI, Takaaki
SAITO, Kazuki
YAMAZAKI, Mami
ZHIZHONG, Gong

<120> GENES ENCODING PROTEINS HAVING TRANSGLYCOSYLATION
ACTIVITY

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<140> 09/147,955

<141> 1999-03-24

<150> PCT/JP98/03199

<151> 1998-07-16

<150> JP 9-200571

<151> 1997-07-25

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<170> PatentIn Ver. 2.0

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Arg	Val	Arg	Ala	Asn	Glu	Glu	Gly	Ser	Val	Val	Val	Asp	Gly	Asp	Glu	Ile	
	395					400					405						
agg	aga	tgt	att	gag	gag	gtt	atg	gat	ggg	gga	gaa	aag	agt	agg	aaa	1300	
Arg	Arg	Cys	Ile	Glu	Glu	Val	Met	Asp	Gly	Gly	Glu	Lys	Ser	Arg	Lys		
410				415					420					425			
ctt	aga	gag	agt	gct	ggc	aag	tgg	aag	gat	ttg	gca	aga	aaa	gct	atg	1348	
Leu	Arg	Glu	Ser	Ala	Gly	Lys	Trp	Lys	Asp	Leu	Ala	Arg	Lys	Ala	Met		
				430					435					440			
gag	gaa	gat	gga	tct	tca	gtt	aac	aac	ctc	aag	gtc	ttt	ctt	gat	gag	1396	
Glu	Glu	Asp	Gly	Ser	Ser	Val	Asn	Asn	Leu	Lys	Val	Phe	Leu	Asp	Glu		
			445					450					455				
gtt	gta	ggt	atc	taaagacgta	aatgagggtcc	ccataggcaa	aattgcaa	aat								1448	
Val	Val	Gly	Ile														
			460														
ttcatctcgt	aagttgaata	ctttttggct	ttaattttgt	tcgagtttgt	ttttcaaaat	1508											
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attcattgtt	gagactcttc	atcaaaatca	tctgattttcc	tttattgtct	tgggtcaaaat	1628											
tctcatatca	attggaaaaa	ataaatttca	aaatcgtcca	attttgaacc	aagaaagaag	1688											
tataatttga	ccaaaataat	aaaaggattc	aagtgatctt	gatgaagtgt	ctgagcgacg	1748											
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gactaacttt	gtacaaaatg	aaaagttata	tgatgaaatt	ttaaaaaaca	aactcagaca	1868											
ataataaagc	ccgaaagtag	taaaattacc	tgacgaaatt	tgcaatttcg	cctcctat	1928											
taattttttt	ggtgtgttta	ataaatcggt	tattttactt	ttaattaaaa	taaaagtgag	1988											
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aaaaaaaaaa	aaaa					2062											

<210> 6
 <211> 461
 <212> PRT
 <213> Verbena hybrida

<400> 6

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Ile Asn Pro Ala Leu Gln Phe Ala Lys Arg Leu Ala Asn Ala Asp Ile
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Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Trp Arg Arg Met Ser Arg
35 40 45
Thr Ala Ala Gly Ser Asn Gly Leu Ile Asn Phe Val Ser Phe Ser Asp
50 55 60
Gly Tyr Asp Asp Gly Leu Gln Pro Gly Asp Asp Gly Lys Asn Tyr Met
65 70 75 80
Ser Glu Met Lys Ser Arg Gly Ile Lys Ala Leu Ser Asp Thr Leu Ala
85 90 95
Ala Asn Asn Val Asp Gln Lys Ser Ser Lys Ile Thr Phe Val Val Tyr
100 105 110
Ser His Leu Phe Ala Trp Ala Ala Lys Val Ala Arg Glu Phe His Leu
115 120 125
Arg Ser Ala Leu Leu Trp Ile Glu Pro Ala Thr Val Leu Asp Ile Phe
130 135 140
Tyr Phe Tyr Phe Asn Gly Tyr Ser Asp Glu Ile Asp Ala Gly Ser Asp
145 150 155 160
Ala Ile His Leu Pro Gly Gly Leu Pro Val Leu Ala Gln Arg Asp Leu
165 170 175
Pro Ser Phe Leu Leu Pro Ser Thr His Glu Arg Phe Arg Ser Leu Met
180 185 190
Lys Glu Lys Leu Glu Thr Leu Glu Gly Glu Glu Lys Pro Lys Val Leu
195 200 205
Val Asn Ser Phe Asp Ala Leu Glu Pro Asp Ala Leu Lys Ala Ile Asp
210 215 220
Lys Tyr Glu Met Ile Ala Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu
225 230 235 240
Asp Gly Lys Asp Pro Ser Asp Arg Ser Phe Gly Gly Asp Leu Phe Glu
245 250 255
Lys Gly Ser Asn Asp Asp Asp Cys Leu Glu Trp Leu Ser Thr Asn Pro
260 265 270
Arg Ser Ser Val Val Tyr Val Ser Phe Gly Ser Phe Val Asn Thr Thr
275 280 285
Lys Ser Gln Met Glu Glu Ile Ala Arg Gly Leu Leu Asp Cys Gly Arg
290 295 300
Pro Phe Leu Trp Val Val Arg Val Asn Glu Gly Glu Glu Val Leu Ile
305 310 315 320
Ser Cys Met Glu Glu Leu Lys Arg Val Gly Lys Ile Val Ser Trp Cys
325 330 335

Ser Gln Leu Glu Val Leu Thr His Pro Ser Leu Gly Cys Phe Val Thr
340 345 350

His Cys Gly Trp Asn Ser Thr Leu Glu Ser Ile Ser Phe Gly Val Pro
355 360 365

Met Val Ala Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys Leu
370 375 380

Met Glu Asp Val Trp Arg Thr Gly Val Arg Val Arg Ala Asn Glu Glu
385 390 395 400

Gly Ser Val Val Asp Gly Asp Glu Ile Arg Arg Cys Ile Glu Glu Val
405 410 415

Met Asp Gly Gly Glu Lys Ser Arg Lys Leu Arg Glu Ser Ala Gly Lys
420 425 430

Trp Lys Asp Leu Ala Arg Lys Ala Met Glu Glu Asp Gly Ser Ser Val
435 440 445

Asn Asn Leu Lys Val Phe Leu Asp Glu Val Val Gly Ile
450 455 460

<210> 7
<211> 1671
<212> DNA
<213> Torenia hybrira

<220>
<221> CDS
<222> (45)..(1478)

<220>
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<222> (64)
<223> Amino acid 64 is Xaa wherein Xaa = Cys or Phe.

<220>
<221> misc_feature
<222> (65)
<223> Amino acid 65 is Xaa wherein Xaa = Ser or Pro.

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Met Val Asn Lys
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cgc cat att cta cta gca aca ttc cca gca caa ggc cac ata aac cct 104
Arg His Ile Leu Leu Ala Thr Phe Pro Ala Gln Gly His Ile Asn Pro
5 10 15 20

tct ctc gag ttc gcc aaa agg ctc ctc aac acc gga tac gtc gac caa 152
Ser Leu Glu Phe Ala Lys Arg Leu Leu Asn Thr Gly Tyr Val Asp Gln
25 30 35

gtc aca ttc ttc acg agt gta tac gca ttg aga cgc atg cgc ttc gaa 200
Val Thr Phe Phe Thr Ser Val Tyr Ala Leu Arg Arg Met Arg Phe Glu
40 45 50

acc gat ccg agc agc aga atc gat ttc gtg gca tkt yca gat tct tac 248
Thr Asp Pro Ser Ser Arg Ile Asp Phe Val Ala Xaa Xaa Asp Ser Tyr

55					60					65						
gat	gat	ggc	tta	aag	aaa	ggc	gac	gat	ggc	aaa	aac	tac	atg	tcg	gag	296
Asp	Asp	Gly	Leu	Lys	Lys	Gly	Asp	Asp	Gly	Lys	Asn	Tyr	Met	Ser	Glu	
	70					75					80					
atg	aga	aag	cgc	gga	acg	aag	gcc	tta	aag	gac	act	ctt	att	aag	ctc	344
Met	Arg	Lys	Arg	Gly	Thr	Lys	Ala	Leu	Lys	Asp	Thr	Leu	Ile	Lys	Leu	
	85				90					95					100	
aac	gat	gct	gcg	atg	gga	agt	gaa	tgt	tac	aat	cgc	gtg	agc	ttt	gtg	392
Asn	Asp	Ala	Ala	Met	Gly	Ser	Glu	Cys	Tyr	Asn	Arg	Val	Ser	Phe	Val	
				105					110					115		
gtg	tac	tct	cat	cta	ttt	tcg	tgg	gca	gct	gaa	gtg	gcg	cgt	gaa	gtc	440
Val	Tyr	Ser	His	Leu	Phe	Ser	Trp	Ala	Ala	Glu	Val	Ala	Arg	Glu	Val	
			120					125					130			
gac	gtg	ccg	agt	gcc	ctt	ctt	tgg	att	gaa	ccg	gct	acg	gtt	ttc	gat	488
Asp	Val	Pro	Ser	Ala	Leu	Leu	Trp	Ile	Glu	Pro	Ala	Thr	Val	Phe	Asp	
		135					140					145				
gtg	tac	tat	ttt	tac	ttc	aat	ggg	tat	gcc	gat	gat	atc	gat	gcg	ggc	536
Val	Tyr	Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ala	Asp	Asp	Ile	Asp	Ala	Gly	
	150					155					160					
tca	gat	caa	atc	caa	ctg	ccc	aat	ctt	ccg	cag	ctc	tcc	aag	caa	gat	584
Ser	Asp	Gln	Ile	Gln	Leu	Pro	Asn	Leu	Pro	Gln	Leu	Ser	Lys	Gln	Asp	
	165				170					175					180	
ctc	ccc	tct	ttc	cta	ctc	cct	tcg	agc	ccc	gcg	aga	ttc	cga	acc	cta	632
Leu	Pro	Ser	Phe	Leu	Leu	Pro	Ser	Ser	Pro	Ala	Arg	Phe	Arg	Thr	Leu	
				185					190					195		
atg	aaa	gaa	aag	ttc	gac	acg	ctc	gac	aaa	gaa	ccg	aaa	gcg	aag	gtc	680
Met	Lys	Glu	Lys	Phe	Asp	Thr	Leu	Asp	Lys	Glu	Pro	Lys	Ala	Lys	Val	
			200					205					210			
ttg	ata	aac	acg	ttc	gac	gca	tta	gaa	acc	gaa	caa	ctc	aaa	gcc	atc	728
Leu	Ile	Asn	Thr	Phe	Asp	Ala	Leu	Glu	Thr	Glu	Gln	Leu	Lys	Ala	Ile	
		215					220					225				
gac	agg	tat	gaa	cta	ata	tcc	atc	ggc	cca	tta	atc	cca	tca	tcg	ata	776
Asp	Arg	Tyr	Glu	Leu	Ile	Ser	Ile	Gly	Pro	Leu	Ile	Pro	Ser	Ser	Ile	
	230					235					240					
ttc	tca	gat	ggc	aac	gac	ccc	tca	tca	agc	aac	aaa	tcc	tac	ggt	gga	824
Phe	Ser	Asp	Gly	Asn	Asp	Pro	Ser	Ser	Ser	Asn	Lys	Ser	Tyr	Gly	Gly	
	245				250					255				260		
gac	ctc	ttc	aga	aaa	gcc	gat	gaa	act	tac	atg	gac	tgg	cta	aac	tca	872
Asp	Leu	Phe	Arg	Lys	Ala	Asp	Glu	Thr	Tyr	Met	Asp	Trp	Leu	Asn	Ser	
				265					270					275		
aaa	ccc	gaa	tca	tcg	gtc	gtt	tac	gtt	tcg	ttc	ggg	agc	ctc	ctg	agg	920
Lys	Pro	Glu	Ser	Ser	Val	Val	Tyr	Val	Ser	Phe	Gly	Ser	Leu	Leu	Arg	
			280					285					290			
ctc	ccg	aaa	ccc	caa	atg	gaa	gaa	ata	gca	ata	ggg	ctt	tca	gac	acc	968
Leu	Pro	Lys	Pro	Gln	Met	Glu	Glu	Ile	Ala	Ile	Gly	Leu	Ser	Asp	Thr	
		295					300					305				
aaa	tcg	cca	gtt	ctc	tgg	gtg	ata	aga	aga	aac	gaa	gag	ggc	gac	gaa	1016

Lys Ser Pro Val Leu Trp Val Ile Arg Arg Asn Glu Glu Gly Asp Glu
 310 315 320
 caa gag caa gca gaa gaa gaa gag aag ctg ctg agc ttc ttt gat cgt 1064
 Gln Glu Gln Ala Glu Glu Glu Glu Lys Leu Leu Ser Phe Phe Asp Arg
 325 330 335 340
 cac gga act gaa cga ctc ggg aaa atc gtg aca tgg tgc tca caa ttg 1112
 His Gly Thr Glu Arg Leu Gly Lys Ile Val Thr Trp Cys Ser Gln Leu
 345 350 355
 gat gtt ctg acg cat aag tgc gtg gga tgc ttc gtg acg cat tgc ggt 1160
 Asp Val Leu Thr His Lys Ser Val Gly Cys Phe Val Thr His Cys Gly
 360 365 370
 tgg aat tct gct atc gag agc ctg gct tgt ggt gtg ccc gtg gtg tgc 1208
 Trp Asn Ser Ala Ile Glu Ser Leu Ala Cys Gly Val Pro Val Val Cys
 375 380 385
 ttt cct caa tgg ttc gat caa ggg act aat gcg aag atg atc gaa gat 1256
 Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys Met Ile Glu Asp
 390 395 400
 gtg tgg agg agt ggt gtg aga gtc aga gtg aat gag gaa ggc ggc gtt 1304
 Val Trp Arg Ser Gly Val Arg Val Arg Val Asn Glu Glu Gly Gly Val
 405 410 415 420
 gtt gat agg cgt gag att aag agg tgc gtc tgc gag gtt ata aag agt 1352
 Val Asp Arg Arg Glu Ile Lys Arg Cys Val Ser Glu Val Ile Lys Ser
 425 430 435
 cga gag ttg aga gaa agc gca atg atg tgg aag ggt ttg gct aaa gaa 1400
 Arg Glu Leu Arg Glu Ser Ala Met Met Trp Lys Gly Leu Ala Lys Glu
 440 445 450
 gct atg gat gaa gaa cgt gga tca tca atg aac aat ctg aag aat ttt 1448
 Ala Met Asp Glu Glu Arg Gly Ser Ser Met Asn Asn Leu Lys Asn Phe
 455 460 465
 att act agg att att aat gaa aat gcc tca taagttgtac tatatatggt 1498
 Ile Thr Arg Ile Ile Asn Glu Asn Ala Ser
 470 475
 attattgttg ttatggacgt cgaattaaagt attagttaaa tgatatgtat ttagaggaag 1558
 gccaaaacgg gctacacccg gcaggccacg gggttgaaaa gcccgccatg atttaaaata 1618
 tatatttttaa aataaatatt ttctactatt aaactaaaaaa aaaaaaaaaaaa aaa 1671

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 <211> 478
 <212> PRT
 <213> Torenia hybrira

<400> 8
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 His Ile Asn Pro Ser Leu Glu Phe Ala Lys Arg Leu Leu Asn Thr Gly
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 Tyr Val Asp Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Leu Arg Arg

35										40					45															
Met	Arg	Phe	Glu	Thr	Asp	Pro	Ser	Ser	Arg	Ile	Asp	Phe	Val	Ala	Xaa															
	50						55				60																			
Xaa	Asp	Ser	Tyr	Asp	Asp	Gly	Leu	Lys	Lys	Gly	Asp	Asp	Gly	Lys	Asn															
	65				70					75					80															
Tyr	Met	Ser	Glu	Met	Arg	Lys	Arg	Gly	Thr	Lys	Ala	Leu	Lys	Asp	Thr															
				85					90					95																
Leu	Ile	Lys	Leu	Asn	Asp	Ala	Ala	Met	Gly	Ser	Glu	Cys	Tyr	Asn	Arg															
			100					105					110																	
Val	Ser	Phe	Val	Val	Tyr	Ser	His	Leu	Phe	Ser	Trp	Ala	Ala	Glu	Val															
			115				120					125																		
Ala	Arg	Glu	Val	Asp	Val	Pro	Ser	Ala	Leu	Leu	Trp	Ile	Glu	Pro	Ala															
	130					135					140																			
Thr	Val	Phe	Asp	Val	Tyr	Tyr	Phe	Tyr	Phe	Asn	Gly	Tyr	Ala	Asp	Asp															
	145				150					155					160															
Ile	Asp	Ala	Gly	Ser	Asp	Gln	Ile	Gln	Leu	Pro	Asn	Leu	Pro	Gln	Leu															
				165					170					175																
Ser	Lys	Gln	Asp	Leu	Pro	Ser	Phe	Leu	Leu	Pro	Ser	Ser	Pro	Ala	Arg															
			180					185					190																	
Phe	Arg	Thr	Leu	Met	Lys	Glu	Lys	Phe	Asp	Thr	Leu	Asp	Lys	Glu	Pro															
	195						200					205																		
Lys	Ala	Lys	Val	Leu	Ile	Asn	Thr	Phe	Asp	Ala	Leu	Glu	Thr	Glu	Gln															
	210					215					220																			
Leu	Lys	Ala	Ile	Asp	Arg	Tyr	Glu	Leu	Ile	Ser	Ile	Gly	Pro	Leu	Ile															
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Pro	Ser	Ser	Ile	Phe	Ser	Asp	Gly	Asn	Asp	Pro	Ser	Ser	Ser	Asn	Lys															
			245						250					255																
Ser	Tyr	Gly	Gly	Asp	Leu	Phe	Arg	Lys	Ala	Asp	Glu	Thr	Tyr	Met	Asp															
			260					265					270																	
Trp	Leu	Asn	Ser	Lys	Pro	Glu	Ser	Ser	Val	Val	Tyr	Val	Ser	Phe	Gly															
	275						280					285																		
Ser	Leu	Leu	Arg	Leu	Pro	Lys	Pro	Gln	Met	Glu	Glu	Ile	Ala	Ile	Gly															
	290					295					300																			
Leu	Ser	Asp	Thr	Lys	Ser	Pro	Val	Leu	Trp	Val	Ile	Arg	Arg	Asn	Glu															
	305				310					315					320															
Glu	Gly	Asp	Glu	Gln	Glu	Gln	Ala	Glu	Glu	Glu	Glu	Lys	Leu	Leu	Ser															
				325					330					335																
Phe	Phe	Asp	Arg	His	Gly	Thr	Glu	Arg	Leu	Gly	Lys	Ile	Val	Thr	Trp															
			340					345					350																	
Cys	Ser	Gln	Leu	Asp	Val	Leu	Thr	His	Lys	Ser	Val	Gly	Cys	Phe	Val															
		355					360					365																		
Thr	His	Cys	Gly	Trp	Asn	Ser	Ala	Ile	Glu	Ser	Leu	Ala	Cys	Gly	Val															

370	375	380
Pro Val Val Cys Phe	Pro Gln Trp Phe Asp	Gln Gly Thr Asn Ala Lys
385	390	395 400
Met Ile Glu Asp Val	Trp Arg Ser Gly Val	Arg Val Arg Val Asn Glu
	405	410 415
Glu Gly Gly Val Val	Asp Arg Arg Glu Ile	Lys Arg Cys Val Ser Glu
	420	425 430
Val Ile Lys Ser Arg	Glu Leu Arg Glu Ser	Ala Met Met Trp Lys Gly
	435	440 445
Leu Ala Lys Glu Ala	Met Asp Glu Glu Arg	Gly Ser Ser Met Asn Asn
	450	455 460
Leu Lys Asn Phe Ile	Thr Arg Ile Ile Asn	Glu Asn Ala Ser
465	470	475

<210> 9
 <211> 1437
 <212> DNA
 <213> *Perilla frutescens*

<220>
 <221> CDS
 <222> (294)..(1298)

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 tcatacctacc agcatcatca tgatcaatct ctttataatg aggagaatgg agtaacaagg 120
 agtggggtttt gttactcagc ttcaacctac gtacgtacta ctactgactc aactotcaag 180
 agaatgaata taatatataa tgggcgatag atctttgtag atatgtagggt gtagcctgca 240
 ggtgggtaat taatttccgg tgtgggaaaa taaataaata aataaatata gcg atg 296
 Met
 1
 agc agc agc agc agc aga agg tgg aga gag aat gag ggg atg cga agg 344
 Ser Ser Ser Ser Ser Arg Arg Trp Arg Glu Asn Glu Gly Met Arg Arg
 5 10 15
 aca ttg ctg ggg ttg ggt ttg ggg cag ttg gtt tct ttc gat ttg gct 392
 Thr Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu Ala
 20 25 30
 atc atg acc ttt tct gct tct ttg gtt tca acc aca gtg gat gca cca 440
 Ile Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala Pro
 35 40 45
 ctt act atg tcg ttc act aca tac act gtt gtg gcc ctg ctc tat gga 488
 Leu Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr Gly
 50 55 60 65
 acc atc ttg ctt tac cgc cgc cac aaa ttc ttg gtt cca tgg tac tgg 536
 Thr Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr Trp
 70 75 80

tat gct ctc ctg ggg ttc gtg gac gtc cac ggc aat tat ctt gtt aat	584
Tyr Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val Asn	
85 90 95	
aaa gca ttc gag ttg aca tcg att acg agt gtg agc ata ctg gat tgt	632
Lys Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp Cys	
100 105 110	
tgg aca atc gtg tgg tcc atc atc ttt aca tgg atg ttc cta ggc aca	680
Trp Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly Thr	
115 120 125	
aaa tac tct gta tac cag ttt gtc ggt gct gct att tgt gta gga ggc	728
Lys Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly Gly	
130 135 140 145	
ctc ctc ctc gtg ctt ctt tcc gac tca ggc gtc act gct gct ggt tcg	776
Leu Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly Ser	
150 155 160	
aat cct ctt ttg ggt gat ttt ctt gtc ata aca ggc tct att ttg ttc	824
Asn Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu Phe	
165 170 175	
aca ctc agc act gtt ggt cag gaa tac tgc gtg aag agg aaa gat cgt	872
Thr Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp Arg	
180 185 190	
att gaa gta gta gca atg atc ggt gta ttt ggt atg ctc atc agt gca	920
Ile Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser Ala	
195 200 205	
acc gag att act gtg ctg gag agg aat gcc ctc tca tca atg cag tgg	968
Thr Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln Trp	
210 215 220 225	
tct act gga ctt ttg gca gcc tat gtt gtt tat gca ctg tcc agc ttc	1016
Ser Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser Phe	
230 235 240	
ctc ttc tgc aca ctc acc cct ttt ctt ctc aag atg agt ggc gct gca	1064
Leu Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala Ala	
245 250 255	
ttt ttc aat ctt tcc atg ctt aca tct gat atg tgg gct gtt gca att	1112
Phe Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala Ile	
260 265 270	
agg aca ttc ata tac aac cag gag gtt gat tgg tta tac tat ttg gcc	1160
Arg Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu Ala	
275 280 285	
ttt tgt ctc gtt gtt gtt gga ata ttc ata tat aca aaa aca gag aag	1208
Phe Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu Lys	
290 295 300 305	
gat cct aac aat acg aga gcc ctt gag aat gga aac ttg gat cat gaa	1256
Asp Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His Glu	
310 315 320	
tat agt ctc ctt gag gat caa gat gac aca cca aga aaa cca	1298
Tyr Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro	
325 330 335	

tagctagctt tgcccacaat cttttcatca acagttttaa ataattcgtg aggggggagag 1358
 agatcgagat actaattaat ggacgtctat tatatagttg gaggtttttg ttttatttat 1418
 ttatttgagt aaaaaaaaaa 1437

<210> 10
 <211> 335
 <212> PRT
 <213> *Perilla frutescens*

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 Arg Thr Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu
 20 25 30
 Ala Ile Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala
 35 40 45
 Pro Leu Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr
 50 55 60
 Gly Thr Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr
 65 70 75 80
 Trp Tyr Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val
 85 90 95
 Asn Lys Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp
 100 105 110
 Cys Trp Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly
 115 120 125
 Thr Lys Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly
 130 135 140
 Gly Leu Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly
 145 150 155 160
 Ser Asn Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu
 165 170 175
 Phe Thr Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp
 180 185 190
 Arg Ile Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser
 195 200 205
 Ala Thr Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln
 210 215 220
 Trp Ser Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser
 225 230 235 240
 Phe Leu Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala
 245 250 255
 Ala Phe Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala
 260 265 270

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